

a.) Amendment to the Claims

1. (Currently Amended) A process for producing an amino acid, which comprises the steps of:

culturing, in a medium, a microorganism expressing a heterologous DNA encoding a NADH dehydrogenase in which the number of protons discharged per electron is zero, said heterologous DNA being (i) SEQ ID NO:3 or (ii) a DNA ~~which hybridizes, under stringent conditions, with a DNA having a nucleotide sequence complementary to the full-length~~ having 95% or more homology to the nucleotide sequence of SEQ ID NO:3,

forming and accumulating an amino acid in a culture, and

recovering the amino acid from the culture;

~~wherein said stringent condition comprise hybridization at 65°C in the presence of 0.7 to 1.0 mol/l NaCl on a filter having fixed DNA followed by washing at 65°C using 0.1 to 2-fold SSC.~~

2. (Previously Presented) The process according to claim 1, wherein the heterologous DNA of (i) or (ii) is derived from a microorganism selected from the group consisting of *Corynebacterium*, *Escherichia*, *Pseudomonas*, *Azotobacter*, *Salmonella* and *Lactobacillus*.

3. (Previously Presented) The process according to claim 2, wherein the heterologous DNA of (i) or (ii) is derived from a microorganism selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium diphtheriae*, *Escherichia coli*, *Pseudomonas fluorescens*, *Azotobacter vinelandii*, *Salmonella typhimurium* and *Lactobacillus plantarum*.

Claim 4 (Cancelled).

5. (Currently Amended) The process according to claim 1, wherein the heterologous DNA of (i) or (ii) is DNA within microorganism comprises the plasmid pCS-CGndh within *Escherichia coli* DH5 $\alpha$ /pCS-CGndh.

6. (Previously Presented) The process according to claim 1, wherein the NADH dehydrogenase is a polypeptide comprising (1) SEQ ID NO:4 or (2) SEQ ID NO:4 wherein 1 to 20 amino acid residues are deleted, substituted or added in the amino acid sequence of the polypeptide.

Claim 7 (Cancelled).

8. (Previously Presented) The process according to claim 1, wherein the microorganism is selected from the group consisting of *Escherichia*, *Corynebacterium*, *Brevibacterium*, *Arthrobacter*, *Aureobacterium*, *Cellulomonas*, *Clavibacter*, *Curtobacterium*, *Microbacterium*, *Pimerobacter* and *Bacillus*.

9. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the genus *Escherichia*.

10. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the species *Escherichia coli*.

11. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the genus *Corynebacterium*.

12. (Previously Presented) The process according to claim 1, wherein the microorganism is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium flavum*, *Corynebacterium lactofermentum*, and *Corynebacterium efficiasis*.

13. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the species *Corynebacterium glutamicum*.

14. (Previously Presented) The process according to claim 1, wherein the amino acid is selected from the group consisting of L-glutamic acid, L-glutamine, L-aspartic acid, L-asparagine, L-lysine, L-methionine, L-threonine, L-arginine, L-proline, L-citrulline, L-valine, L-leucine, L-isoleucine, L-serine, L-cysteine, glycine, L-tryptophan, L-tyrosine, L-phenylalanine and L-histidine.

15. (Previously Presented) The process according to claim 1, wherein the amino acid is selected from the group consisting of L-glutamic acid, L-glutamine and L-lysine.

Claims 16-26 (Cancelled).